



#9
Elaborata
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

STEPHEN M. ALLEN

ATTY. DOCKET NO.: BB1170 USCIP

APPLICATION NO.: 09/900,237

GROUP ART UNIT: 1638

FILED: JULY 6, 2001

EXAMINER: BUI, PHUONG T.

CONFIRMATION NO.: 4901

FOR: PLANT CELLULOSE SYNTHASES

**PRELIMINARY AMENDMENT
AND RESPONSE TO RESTRICTION REQUIREMENT**

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

This is a Preliminary Amendment and Response to the Restriction Requirement set forth in the Office Action mailed September 27, 2002. A Petition for Extension of Time for three (3) month up to and including January 27, 2003, is filed simultaneously herewith. Please enter the following:

IN THE SPECIFICATION:

Please amend the specification as follows; a marked-up version showing changes made is attached hereto:

Paragraph at page 10, lines 9-31:

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A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or